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ID   AB211185 standard; cDNA; 5166 BP.
XX
AC   AB211185;
XX
DT   20-JAN-2003 (first entry)
XX
DE   Human polynucleotide SEQ ID NO 67.
XX
KW   Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW   cell-proliferative disorder; neurodegenerative disease; bacterial;
KW   Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW   multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW   arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW   antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW   haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW   antiarthritic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200270539-A2.
XX
PD   12-SEP-2002.
XX
PF   05-MAR-2002; 2002WO-US005095.
XX
PR   05-MAR-2001; 2001US-00799451.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI   Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI   Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR   WPI; 2002-759812/82.
DR   P-PSDB; ABP68968.
XX
PT   New polynucleotides comprising sequences assembled from expressed
PT   sequence tags (ESTs), useful for treating cell-proliferative,
PT   neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT   or coagulation disorders.
XX
PS   Claim 1; SEQ ID NO 67; 1012pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising a
CC   nucleotide sequence selected from any of 948 sequences (AB211119-
CC   AB212066) or their mature protein coding portion, active domain coding
CC   protein or complementary sequences. The polynucleotides are useful for
CC   identifying expressed genes or for physical mapping of human genome. The
CC   encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC   markers, as a food supplement, for generating antibodies, in medical
CC   imaging, screening and diagnostic assays and for treating cell-
CC   proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC   or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC   diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC   platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC   or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC   arthritis, etc. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5166 BP; 1108 A; 1674 C; 1483 G; 901 T; 0 U; 0 Other;

Query Match       96.9%;  Score 4301.8;  DB 6;  Length 5166;
Best Local Similarity  98.8%;  Pred. No. 0;
Matches 4367;  Conservative  0; Mismatches  17; Indels  35; Gaps  2;

Qy         46 CTCGGAGTGAGTTCCCAGACCCTACCCCCCCGTGTCAGCCAGCCCGGATCCAGGATGGA 105
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Qy        106 GGAGAACGAGGTGGAGAGCAGCAGCGACGCGGCCCCTGGCCGGCCCGGGCGGCGGAGAGCC 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 GGAGAACGAGGTGGAGAGCAGCAGCGACGCGGCCCCTGGCCGGCCCGGGCGGCGGAGAGCC 499
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The right-side aligned sequence block (rotated column):

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Qy   3461 CACATCCAGCGGCTGCACAGTCCTGATGGGAGTCAGGAACCCCTACAGCCCGGGCC 3520
Db   3361 CACATCCAGCGGCTGCACAGTCCTGATGGGAGTCAGGAACCCCTACAGCCCGGGCC 3420
Qy   3521 CCTACCCAGACCCCAACCCAGACCATCATCCTGAACACAGTGATGACGAAACACTGGCCACC 3580
Db   3421 CCTACCCAGACCCCAACCCAGACCATCATCCTGAACACAGTGATGACGAAACACTGGCCACC 3480
Qy   3581 CTGCACACTGCACTCCAGTCCAGCGGGTCCTGGGCCCAGAGCGGCTACAGCAGCA 3640
Db   3481 CTGCACACTGCACTCCAGTCCAGCGGGTCCTGGGCCCAGAGCGGCTACAGCAGCA 3540
Qy   3641 CTGAGGCCAGGAACACATCATCGTTGCCCAGGAACAGACAGATCAGGAGGAAGCC 3700
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Qy   3881 CAGTATGAACAAGGAGGAGCCCCGGTTCCTTCAGGAGTCCCAGATCCAGTATGTGCCTGTGTCC 3940
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Qy   4421 AACAGCTTAAAAAAAAAA 4439
Db   4321 AACAGCTTAAAAAAAAAA 4339

RESULT 4
AB211185
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                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April  7, 2006, 22:17:45 ; Search time 503.168 Seconds
                                      (without alignments)
                                   15681.845 Million cell updates/sec

Title:          US-10-645-250A-1
Perfect score:  4439
Sequence:       1 gacctcgtcgatgccggagt.........gaacagcttaaaaaaaaaa 4439

Scoring table:  IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:       2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	4301.8	96.9	5166	3	US-09-799-451-67	Sequence 67, Appl
2	822.6	18.5	1396	3	US-10-104-047-1092	Sequence 1092, Ap
3	91.8	2.1	2141	3	US-09-774-528-373	Sequence 373, App
4	91.8	2.1	2141	3	US-10-120-988-373	Sequence 373, App
5	76.2	1.7	2775	3	US-09-774-528-170	Sequence 170, App
6	76.2	1.7	2775	3	US-10-120-988-170	Sequence 170, App
7	73.2	1.6	2680	3	US-09-063-035-1	Sequence 1, Appli
8	73.2	1.6	2769	3	US-09-620-312D-309	Sequence 309, App
9	71.8	1.6	993	3	US-09-949-016-3977	Sequence 3977, Ap
10	71.8	1.6	2416	3	US-09-016-434-1058	Sequence 1058, Ap
11	71.2	1.6	2954	3	US-09-477-392-1	Sequence 1, Appli
12	71.2	1.6	2954	3	US-09-477-391-1	Sequence 1, Appli
13	69.8	1.6	1892	2	US-08-933-750C-66	Sequence 66, Appl
14	69.8	1.6	1892	3	US-09-234-613-66	Sequence 66, Appl
15	69.4	1.6	2550	3	US-09-949-016-4927	Sequence 4927, Ap
16	69.4	1.6	2850	2	US-08-224-482-7	Sequence 7, Appli
17	69.4	1.6	3818	3	US-09-949-016-5445	Sequence 5445, Ap
18	69.4	1.6	4289	3	US-09-949-016-627	Sequence 627, App
19	69.4	1.6	10106	3	US-09-949-016-17187	Sequence 17187, A
20	69.4	1.6	27933	3	US-09-949-016-12369	Sequence 12369, A
21	69.2	1.6	2678	3	US-09-016-434-1229	Sequence 1229, Ap
22	68.2	1.5	2336	3	US-10-104-047-1925	Sequence 1925, Ap
23	68.2	1.5	2459	3	US-09-799-451-853	Sequence 853, App
24	67.6	1.5	2643	3	US-09-016-434-1398	Sequence 1398, Ap
25	67.6	1.5	2643	3	US-09-949-016-486	Sequence 486, App
26	67.2	1.5	1371	3	US-09-389-956-67	Sequence 67, Appl
27	67.2	1.5	2262	3	US-09-389-956-5	Sequence 5, Appli
28	66.8	1.5	2165	3	US-09-949-016-1613	Sequence 1613, Ap
29	66.8	1.5	15331	3	US-09-949-016-13355	Sequence 13355, A
30	66.2	1.5	1558	3	US-09-620-312D-32	Sequence 32, Appl
31	65.4	1.5	4252	2	US-08-475-844-4	Sequence 4, Appli
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33	65	1.5	2992	3	US-09-362-123A-3	Sequence 3, Appli
34	64.8	1.5	1964	3	US-09-774-528-308	Sequence 308, App
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36	64.4	1.5	3777	3	US-09-121-321-15	Sequence 15, Appl
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38	64.2	1.4	2301	3	US-09-774-528-110	Sequence 110, App
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44	61.6	1.4	2948	3	US-09-774-528-145	Sequence 145, App
45	61.6	1.4	2948	3	US-10-120-988-145	Sequence 145, App

ALIGNMENTS

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RESULT 1
US-09-799-451-67
; Sequence 67, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 67
; LENGTH: 5166
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (794)..(4495)
US-09-799-451-67

Query Match            96.9%;  Score 4301.8;  DB 3;  Length 5166;
Best Local Similarity  98.8%;  Pred. No. 0;
Matches 4367;  Conservative 0;  Mismatches 17;  Indels 35;  Gaps 2;

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